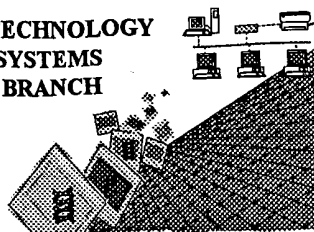


0300

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/852,058 A
Source: OIP
Date Processed by STIC: 3/27/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/852,058A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 26 (and more) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OICE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/852,058A

DATE: 03/27/2002
 TIME: 14:34:28

Input Set : A:\EP.txt
 Output Set: N:\CRF3\03272002\I852058A.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Diatech Pty. Ltd.
 4 <120> TITLE OF INVENTION: A method
 6 <130> FILE REFERENCE: 2414905/EJH
 8 <140> CURRENT APPLICATION NUMBER: US 09/852,058A
 9 <141> CURRENT FILING DATE: 2001-05-09
 11 <150> PRIOR APPLICATION NUMBER: US 60/202,797
 12 <151> PRIOR FILING DATE: 2000-05-09
 14 <160> NUMBER OF SEQ ID NOS: 26
 15 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

219 <210> SEQ ID NO: 26
 220 <211> LENGTH: 30
 221 <212> TYPE: DNA
 222 <213> ORGANISM: artificial sequence
 W--> 224 <220> FEATURE:
 W--> 224 <223> OTHER INFORMATION:
 224 <400> SEQUENCE: 26
 225 atcgcgaaaa ctgtggaatt gatcagcggt
 E--> 227 a:\2414905.diatech.method.doc-3/27/02
 E--> 232 - i -

(global error)

→ see item 11 on Error
 Summary Sheet

30

The types of errors shown exist throughout
 the Sequence Listing. Please check all
 sequences for similar errors.

delete

VERIFICATION SUMMARY

DATE: 03/27/2002

PATENT APPLICATION: US/09/852,058A

TIME: 14:34:29

Input Set : A:\EP.txt

Output Set: N:\CRF3\03272002\I852058A.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:22 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:22 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:30 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:30 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:38 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:38 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:47 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:47 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:55 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:55 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:63 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:63 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:71 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:71 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:87 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:103 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:111 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:120 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:120 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:128 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:128 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:144 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:152 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:160 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:168 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:168 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:176 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:176 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:184 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:184 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:192 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:192 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:200 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:200 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:208 M:258 W: Mandatory Feature missing, <220> FEATURE:

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/852,058A

DATE: 03/27/2002

TIME: 14:34:29

Input Set : A:\EP.txt

Output Set: N:\CRF3\03272002\I852058A.raw

L:208 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:216 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:216 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:227 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:55 SEQ:26
L:227 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:23
L:227 M:112 C: (48) String data converted to lower case,
L:232 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:232 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:55 SEQ:26